



EXHIBIT A

>Monday, March 21, 2005

>DNA59844 [Full]

>685 sites [All Sites]

[DNA59844], avagts (oligo)

[DNA59844], sheldens

> Lib309

tail

snabi

nlalii thal maeli/hpyCH4IV

sphi fnudII/mvni

nsphi bstUI

hpy99I hpyCH4V rsal

tail nspl bsh1236I

hnlII/acyI cac8I csp6I

sapi alui ahaliI/bsaHI mlui bsaAI

mboII aaliiI cac8I aflIII alui apoi

sfcI earI/ksp632I maeli/hpyCH4IV bsIW/spII hpy188I

1 GACACTATATAG AAGAGCTATG ACCTCGCATG CACGCGTAC TAAGCTGGA ATTGGCTCG AGCAGGATGC AGGGCGGCGT GCGAGGAGC TGCCTCTC

CTGTGATATC TTCTCGATAC TGCAGCGTAC GTGCGCATGC ATTGAGCCT TAAGCCGAGC TCGTCTTACG TCCCGGCGCA CCGTCCCTCG ACGGAGGAG

1

M Q G R V A G S C A P L

^Insert starts here

^MET

59844.AV393.f, Stag=TTTTTGAATTCTAAACCAAC^

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scrFI[dcm-]      haeIII/palI
pspGI            stuI[dcm-]
mvaI             scrFI[dcm-]
ecorII[dcm-]     pspGI
dsav[dcm-]       mvaI          bsaXI
bstNI            ecorII[dcm-]  mspI
bssKI[dcm-]      dsav[dcm-]    hpaII
bsII[dcm-]       mboII          scrFI[M.hpaII-]
cac8I apyI[dcm+] bssKI[dcm-]  nciI
haeIII/palI      apyI[dcm+]    dsav      mnII
sau96I[M.haeIII-] bbsI        bsaJI mnII  bssKI sfaNI bseRI
101 TGGGCCTGCT CTTCATCTCC CAGGCCTCTT TGCCCGGAGC ATCGGTGTTG TGGAGGAGAA AGTTTCCCAA AACTTCGGGA CCAACTTGCC
    ACCCGGACGA GGACCAGACA GAAGTAGAGG GTCCGGAGAA ACGGCCTCG TAGCCACAAC ACCTCCTCTT TCAAGGGTT TTGAAGCCTT GGTGAACGG
13  G L L L V C L H L P G L F A R S I G V V E E K V S Q N F G T N L P
    ^59844.AV395.Ef, 5tag=TTTTTATGCATCAGATGACGATGACAAA

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[illegible]

GSeqEdit, DNA59844 [Full], page 3

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sau3AI
mboI/ndeII[dam-]
dpnII[dam-]
dpnI[dam+]
nlaIV
bstYI/xhoII
bamHI
alwI[dam-]
mnlI styI
ddeI alwI[dam-]
bspcNI bsajI
401 CTGAGGATCC TTGGCAGATG ATGGCTGCTG CGGCTGAGGA CCGCCTGGGG GAAGCGCTGC CTGAAGAACT CTCTTACCTC TCCAGTCTG CGGCCCTCGC
GACTCCTAGG AACCGTCTAC TACCGACGAC GCCGACTCCT GCGGACCCCC CTTCGCGAGG GACTTCTTGA GAGAATGGAG AGGTACACGAC GCGGGGAGCG
113 E D P W Q M M A A A E D R L G E A L P E E L S Y L S S A A A L A

scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
tseI sau96I dsav[dcM-] tseI
fnu4HI/bsoFI bstNI fnu4HI/bsoFI
bbvI avall bssKI[dcM-] bbvI
tseI ddeI bsaJI hinPI
mwoI fnu4HI/bsoFI apyI[dcM+] hhaI/cfoI mboII
fnu4HI/bsoFI mnlI bslI haeII eco57I
bbvI acII bspcNI acII afeI/eco47III
401 CTGAGGATCC TTGGCAGATG ATGGCTGCTG CGGCTGAGGA CCGCCTGGGG GAAGCGCTGC CTGAAGAACT CTCTTACCTC TCCAGTCTG CGGCCCTCGC
GACTCCTAGG AACCGTCTAC TACCGACGAC GCCGACTCCT GCGGACCCCC CTTCGCGAGG GACTTCTTGA GAGAATGGAG AGGTACACGAC GCGGGGAGCG
113 E D P W Q M M A A A E D R L G E A L P E E L S Y L S S A A A L A

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scrFI[dcM-]      pleI
pspGI            mlyI
mvaI            hinfI
ecORI[dcM-]      scrFI[dcM-]
dsaV[dcM-]      pspGI
mboII           mvaI
ecORI[dcM-]      ecorII[dcM-]
dsaV[dcM-]      dsaV[dcM-] pleI
bstNI bpuaI     bstNI hpy188I
bssKI[dcM-]     ddeI
bsaJI pleI      bspCNI mnlI hpy188I
apyI[dcM+]     eco8II econI bssKI[dcM-] hpy188III
sau96I(M.haeIII-) bbsI mnlI bsu36I/mstII/sauI bslI[dcM-] mlyI
haeIII/palI     haeIII/palI bslI[dcM-] ahdI/eam1105I
sfanI           bseRI apyI[dcM+] hinfI
hpy188III       stuI hphI mnlI
bslI[dcM-] hinfI
TCCGGGCAGT GGCCTTTGC CTGGGGAGTC GCCACAGGCC TCTCACCTGA GGCTTCACTC CTCCACCAGG ACTCGGAGTC CAGACGACTG
AGGCCCGTCA CCGGGAACG GACCCCTCAG AAGAGGGCTA CCGTGTCGG AGAGTGGACT CCGAAGTCAG GAGGTGGTCC TGAGCCTCAG GTCTGCTGAC
146 P G S G P L P G E S S P D A T G L S P E A S L L H Q D S E S R R L
501

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scrFI[dcM-]
pspGI
mvaI   rsaI
ecorII[dcM-]
dsaV[dcM-]
bstNI  csp6I
bssKI[dcM-]
bsaJI  nlaIV
bsaJI  kpnI
        hphI apyI[dcM+]
sau3AI[M.hphI-]
mboI/ndeII[dcM-]
dpnII[dcM-]  banI
dpnI[dcM+]  asp718
        bclI[dcM-]  acc65I
601 CCCCGTTCTA ATTCACTGGG AGCCGGGGGA AAAATCCTTT CCCAAGCCCT TCCCTGGTCT CTCATCCACA GGGTTCTGCC TGATCACCCC TGGGGTACCC
GGGGCAAGAT TAAGTGACCC TCGGCCCCCT TTTTAGGAAA GGGTTGGGG AGGACACCAGA GAGTAGGTGT CCCAAGACCG ACTAGTGGGG ACCCATGGG
179 P R S N S L G A G G K I L S Q R P P W S L I H R V L P D H P W G T L

        bsmAI
        bsal
scrFI[dcM-]
pspGI
mvaI
        ecorII[dcM-]
dsaV[dcM-]
bstNI
bssKI[dcM-]
bsaJI  foki
        mnlI apyI[dcM+]  bstF5I
scrFI[M.hpall-]
ncII
mspI
hpall
dsaV
bsrI  bssKI
tspRI  bsaJI
        tsp509I  nlaIV

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bsmFI
scrFI[dcn-]
pspGI
mvaI
ecorII[dcn-]
dsaV[dcn-]
bstNI
bssKI[dcn-]
bslI[dcn-]
bsaJI
    apyI[dcn+]
sau96I[dcn-][M.haeIII-]
    mnlI
    haeIII/palI
    bspCNI tfil
    hinfI
    bsaJI
    mnlI
    ecoO109I/draII[dcn-]
    mnlI
    bsaJI
    bsrI
    bsrI
    nlaIII
    bsu36I/mstII/sauI
701 TGAATCCAG TGTCTCTGG GGAGGTGGAG GCCTGGGAC TGGTTGGGA ACAGGCCCA TGCACACCC TGAGGGAATC TGGGGTATCA ATATCAACC
    ACTTAGGGTC ACACAGGACC CCTCCACCTC CGGACCCCTG ACCAACCCCT TGCTCCGGGT ACGGTGTGGG ACTCCCTTAG ACCCATAGT TATTAGTTGG
213 N P S V S W G G G P G T G W G T R P M P H P E G I W G I N N Q P

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rsal
csp6I
nlaIV
kpnI
bani
asp718[dcM-]
acc65I[dcM-]
xcmI
scrFI[dcM-]
pspGI
mvaI
ecoRII[dcM-]
dsaV[dcM-]
bstNI
bssKI[dcM-]
tru9I
apyI[dcM+]
bsaJI
mspAII/nspBII
aseI/asnI/vspI
bcIbI
nmlI
alul
801 CCCAGGTACC AGCTGGGGA ATATTATCG GTATCCAGGA GGCAGCTGGG GAAATATTAA TCGGTATCCA GGAGGCAGCT GGGGGAATAT TAATCGGTAT
GGGTCCATGG TCGACCCCTT TATAATTAGC CATAGTCTCT CCGTCGACCC CTTATAATT AGCCATAGGT CCTCCGTCGA CCCCCTTATA ATTAGCCATA
246 P G T S W G N I N R Y P G G S W G N I N R Y
xcmI pvuII[M.HI-]
scrFI[dcM-]
pspGI mspAII/nspBII
mvaI tseI
ecoRII[dcM-]
dsaV[dcM-]
bstNI fnu4HI/bsoFI
bssKI[dcM-]
tru9I
msei
aseI/asnI/vspI
bcIbI
bbvI
mnII
alul
sspl
bcIbI

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pvuII[M.HI-]
mnli aluI
xcmI mspAII/nbspII
scrFI[dcM-]
pspGI tseI
mvaI fnu4HI/bsoFI
ecoRII[dcM-]
dsaV[dcM-]
bstNI bbvI
bssKI[dcM-]
apyI[dcM+] sspI
xmaI
maei
bfaI
styI
bsaJI
blnI
avrII[dam-]
mnli
1001 CTGGCTTCCC TAATCCTCCA AGCCCTAGGT TGCAGTGGG CTAGAGCAGC ATAGAGGGAA ACCCAACATT GGGAGTTAGA GTCTTGCTCC CGCCCCCTTGC
GACCGAAGGG ATTAGAGGT TCGGGATCCA AGTCACCCC GATCTCGTC TATCTCCCTT TGGGTGTAA CCCTCAATCT CAGGACGAGG CGGGGGAACG
313 G F P N P P S P R L Q W G O
^59844.AV394.r
^59844.AV396.er, 5tag=TTTTTGTGGGCGCGCTTA

sau96I[dcM-](M.haeIII-)

haeIII/palI

eco0109I/draII[dcM-]

alwNI[dcM-]

alw26I/bsmAI

scrFI[dcM-] pciI

pspGI nspHI

mvaI hpaI nlaIII

ecoRII[dcM-] nspI

dsaV[dcM-] tru9I

bsp1286 bstNI hincII/hindII

bmyI bssKI[dcM-] aflIII

banII apyI[dcM+] mseI

mwoI

tspRI mnlI

1101 TGTGTGGGCT CAATCCAGGC CCTGTTAACA TGTTCACG ACTATCCCA CTTTCAGTG CCTCCCTGC TCATCTCAA TAAATAAAA GCATTATGA
ACACACCCGA GTTAGTCCG GGACAATTGT ACAAAGGTCT TGATAGGGT GAAAGTCAC GGAGGGGACG AGTAGAGGTT ATTTTATTTT CGTGAATACT

mc
ea
ea
cf
bs
not
fnu
aci

1201 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

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scrFI[M.hpaII-]
ncII
mspI
hpaII
dsaV          rsaI
xmaI/pspAI    sau96I
smaI          mroI    nlaIV
scrFI[M.hpaII-] rsrII/cspI
ncII          hpy188III csp6I
dsaV          bspMII kpnI
alul salI bsaKI      bspEI banI sfcI
sstI hincII/hindII[M.taqI-] avaiI[M.hpaII-]
sacI accI[M.taqI-] tru9I cpoI asp718 cac8I
rmaI hgiAI/aspHI[M.aluI-] mseI bsaWI cfr10I/bsrFI
maeI ecl136II bsaJI aseI/asnI/vspI acc65I hpyCH4V
bfai bsp1286[M.aluI-] xmnI tsp509I bsaWI pstI
acII speI bsiHKAI taqI bsaKI tsp509I mspI ageI sse8387I
fnu4HI/bsoFI bmyI hpy99I avaiI[M.hpaII-] hpaII mspI bspMI rsaI
haeIII/palI banII[M.aluI-] asp700 accIII hpaII sbfI csp6I aluI sfcI hinfI aluI
1301 GCGCGCGGAC TAGTGAGCTC GTCGACCGCG GAATTAATTC CGGACCGGTA CCTGCAGGCG TACCAGCTTT CCTATAGTG AGTCGTATTA GAGCTTGG
CCGCGGGGCTG ATCACTCGAG CAGCTGGGCC CTTAATTAAG GCCTGGCCAT GGAGTCCGC ATGCTCGAAA GGGATATCAC TCAGCATAAT CTCGAACC

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> length: 1398

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aatII(GACGTC):      20
acc65I(GGTACC):    694 805 1347
accI(CTMKAC):      1321
accIII(TCCGGA):    1339

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aciI (CCGC) : 75 247 254 430 441 490 969 1090 1299 1303
acyI (GRCGYC) : 20
afeI (AGCGCT) : 453
aflIII (ACRYGT) : 32 1128
ageI (ACCGGT) : 1344
ahaII (GRCGYC) : 20
ahdI (GACNNNNNGTC) : 262 580
aluI (AGCT) : 14 43 88 203 299 811 844 877 910 999 1316 1365 1392
alw26I (CAGNNNCTG) : 1116
alwI (GGATCNNNN) : 405 406
alwNI (CAGNNNCTG) : 1116
apoI (RAATTY) : 49
apyI (CCWGG) : 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
1115
aseI (ATTAAT) : 823 856 889 1333
asnI (ATTAAT) : 823 856 889 1333
asp700 (GAANNNTTC) : 1331
asp718 (GTACC) : 694 805 1347
aspHI (GWGCWC) : 1044 1315
avaI (CYCGRG) : 57 1326
avaII (GWCC) : 188 261 438 1342
avrII (CCTAGG) : 265 1024
baeI (NNNNNNNNNNNACNNNGTAYCNNNNNNNNNNN) : 932
bamHI (GGATCC) : 405
banI (GGYRCC) : 694 805 1347
banII (GRCGYC) : 1106 1315
bbsI (GAAGACNNNNN) : 119 528
bbvI (GCACC) : 89 249 375 424 427 456 487 842 875 908
59 752
bcgI (NNNNNNNNNCGANNNNNTGCNNNNNNNNNNN) :
bcivI (GTATCC) : 831 864 897

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| | |
|---------------------------------------|------------------------------------------------------------------|
| bclI (TGATCA) : | 681 |
| bfaI (CTAG) : | 266 1025 1041 1310 |
| bglI (GCNNNNNGGC) : | 971 |
| blnI (CCTAGG) : | 265 1024 |
| blpI (GCTNAGC) : | 300 |
| bmyI (GDGCHC) : | 1044 1106 1315 |
| bpmI (CTGGAG) : | 480 959 |
| bpu1102I (GCTNAGC) : | 300 |
| bpuAI (GAAGACNNNNNN) : | 119 528 |
| bsaAI (YACGTR) : | 37 |
| bsaHI (GRCGYC) : | 20 |
| bsaI (GGTCTCNNNN) : | 656 |
| bsaJI (CCNNGG) : | 129 265 383 409 444 520 623 652 688 689 716 732 733 801 933 1024 |
| | 1326 |
| bsaWI (WCCGGW) : | 1339 1344 |
| bsaXI (NNNNNNNNNACNNNNCTCCNNNNNNNN) : | 146 1072 |
| bseRI (GAGGAGNNNNNNNN) : | 95 163 568 |
| bsgI (GTGCAG) : | 349 |
| bsh1236I (CGCG) : | 33 76 |
| bsiEI (CGRYCG) : | 1300 |
| bsiHKAI (GWGCWC) : | 1044 1315 |
| bsiWI (CGTACG) : | 35 |
| bslI (CCNNNNNNGG) : | 105 199 313 328 331 364 441 495 502 514 570 576 733 1062 1063 |
| bsmAI (GTCTC) : | 657 |
| bsmAI (GTCTC) : | 657 |
| bsmFI (GGGACNNNNNNNNNN) : | 187 736 |
| bsoFI (GCNGC) : | 74 89 249 375 424 427 430 456 487 490 842 875 908 1299 1302 |
| bsp1286 (GDGCHC) : | 1044 1106 1315 |
| bspCNI (CTCAGNNNNNNNN) : | 200 301 401 434 557 770 |
| bspEI (TCCGGA) : | 1339 |

bspMI (ACCTGC): 330 1350
 bspMII (TCCGGA): 1339
 bsrBI (GAGCGG): 254
 bsrFI (RCCGGY): 1344
 bsrI (ACTGNN): 223 482 615 707 739
 bssKI (CCNGG): 111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901
 934 958 976 1115 1326 1327
 bstDSI (CCRYGG): 383
 bstF5I (GGATG): 65 244 663 993
 bstNI (CCWGG): 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976
 1115
 bstUI (CGCG): 33 76
 bstYI (RGATCY): 405
 bsu36I (CCTNAGG): 400 556 769
 btgI (CCRYGG): 383
 btsI (GCAGTGNN): 346 506 1032
 cac8I (GCNNGC): 26 30 104 252 305 378 1000 1354
 cellI (GCTNAGC): 300
 cfoI (GCGC): 92 454
 cfr10I (RCCGGY): 1344
 cfrI (YGGCCR): 1300
 cpoI (CGGWCCG): 1341
 csp6I (GTAC): 36 695 806 1348 1360
 cspi (CGGWCCG): 1341
 ddeI (CTNAG): 200 301 401 434 557 770
 dpnI (GATC): 406 682
 dpnII (GATC): 406 682
 draII (RGGNCCY): 729 1117
 dsal (CCRYGG): 383
 dsav (CCNGG): 111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901

| | |
|--------------------------|---------------------------------------------------------------------|
| eaeI (YGGCCR) : | 934 958 976 1115 1326 1327 |
| eagI (CGGCGG) : | 1300 |
| eam1105I (GACNNNNNGTC) : | 1300 |
| earI (CTCTTCNNNN) : | 262 580 |
| ecfI (GGCGGA) : | 10 981 |
| ecf136II (GAGCTC) : | 968 |
| ecfXI (CGGCGG) : | 1315 |
| eco47III (AGGCT) : | 1300 |
| eco57I (CTGAAG) : | 453 |
| eco81I (CCTNAGG) : | 295 461 |
| ecoNI (CCTNNNNNAGG) : | 400 556 769 |
| ecoO109I (RGGNCCY) : | 331 570 |
| ecori (GAATTC) : | 729 1117 |
| ecorII (CCWGG) : | 49 |
| espI (GCTNAGC) : | 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976 |
| fnu4HI (GCNGC) : | 1115 |
| fnuDII (CGCG) : | 300 |
| fokI (GGATG) : | 74 89 249 375 424 427 430 456 487 490 842 875 908 1299 1302 |
| gsuI (CTGGAG) : | 33 76 |
| haeII (RGCICY) : | 65 244 663 993 |
| haeIII (GGCC) : | 480 959 |
| hgiAI (GNGCWC) : | 453 |
| hhaI (GCGC) : | 73 103 133 226 359 395 492 511 547 730 755 1118 1301 |
| hinPI (GCGC) : | 1044 1315 |
| hincII (GTYRAC) : | 92 454 |
| hindII (GTYRAC) : | 92 454 |
| hinfI (GATC) : | 1124 1321 |
| hinII (GRCGYC) : | 1124 1321 |
| | 388 526 580 586 702 776 1079 1380 |
| | 20 |

| | |
|------------------------|---------------------------------------------------------------------|
| hpaI (GTTAAC) : | 1124 |
| hpaII (CCGG) : | 144 502 623 1327 1340 1345 |
| hphI (GGTGA) : | 553 684 |
| hpy188I (TCNGA) : | 46 206 238 294 316 583 |
| hpy188III (TCNNGA) : | 185 258 534 589 1339 |
| hpy99I (CGWCG) : | 22 1320 |
| hpyCH4IV (ACGT) : | 21 38 |
| hpyCH4V (TGCA) : | 29 68 333 345 350 1031 1353 |
| kpnI (GGTACC) : | 694 805 1347 |
| ksp632I (CTCTTCNNNN) : | 10 981 |
| maeI (CTAG) : | 266 1025 1041 1310 |
| maeII (ACGT) : | 21 38 |
| mboI (GATC) : | 406 682 |
| mboII (GAAGA) : | 10 120 463 529 982 |
| mcrI (CGRYCG) : | 1300 |
| mluI (ACGCGT) : | 32 |
| mlyI (GAGTCNNNN) : | 526 580 586 1079 1380 |
| mnII (CCTC) : | 97 135 163 199 218 230 292 310 338 354 361 403 436 477 495 549 559 |
| | 570 649 722 728 753 772 839 872 905 955 973 1015 1054 1161 |
| mroI (TCCGGA) : | 1339 |
| mseI (TTAA) : | 824 857 890 1125 1334 |
| mspAI (CMGCKG) : | 810 843 876 909 998 |
| mspI (CCGG) : | 144 502 623 1327 1340 1345 |
| mstII (CCTNAGG) : | 400 556 769 |
| mvaI (CCWGG) : | 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976 |
| | 1115 |
| mvnI (CGCG) : | 33 76 |
| mwoI (GCNNNNNNNGC) : | 300 351 424 490 971 1099 1160 |
| ncII (CCSGG) : | 143 502 623 1326 1327 |
| ncoI (CCATGG) : | 383 |

| | |
|----------------------|---------------------------------------------------------------------|
| ndeII (GATC) : | 406 682 |
| nlaIII (CATG) : | 27 384 759 1129 |
| nlaIV (GGNCC) : | 187 226 261 288 395 405 619 694 805 1347 |
| notI (GGGCGCG) : | 1299 |
| nspBII (CMGCKG) : | 810 843 876 909 998 |
| nspHI (RCATGY) : | 26 1128 |
| nspI (RCATGY) : | 26 1128 |
| paer7I (CTCGAG) : | 57 |
| pali (GGCC) : | 73 103 133 226 359 395 492 511 547 730 755 1118 1301 |
| pciI (ACATGT) : | 1128 |
| pflMI (CCANNNNTGG) : | 313 |
| pleI (GATCNNNN) : | 526 580 586 1079 1380 |
| pspAI (CCCGGG) : | 1326 |
| pspGI (CCWGG) : | 111 130 392 444 520 576 653 689 716 733 802 835 868 901 934 958 976 |
| | 1115 |
| pstI (CTGCAG) : | 332 344 1352 |
| pvuII (CAGCTG) : | 810 843 876 909 998 |
| rmaI (CTAG) : | 266 1025 1041 1310 |
| rsaI (GTAC) : | 36 695 806 1348 1360 |
| rsrII (CGGWCCG) : | 1341 |
| sacI (GAGCTC) : | 1315 |
| sali (GTCGAC) : | 1321 |
| sapI (GCTCTTCNNNN) : | 10 980 |
| sau3AI (GATC) : | 406 682 |
| sau96I (GGNCC) : | 72 102 188 226 261 395 438 492 511 730 755 1118 1342 |
| sauI (CCTNAGG) : | 400 556 769 |
| sbfI (CCTGCAGG) : | 331 1351 |
| scrFI (CCNGG) : | 111 130 143 392 444 502 520 576 623 653 689 716 733 802 835 868 901 |
| | 934 958 976 1115 1326 1327 |
| sfaNI (GCATC) : | 66 149 538 |

| | |
|-------------------------|----------------------------------------|
| sfcI (CTRYAG) : | 5 332 344 1352 1373 |
| smaI (CCCGGG) : | 1326 |
| smlI (CTYRAG) : | 57 |
| snaBI (TACGTA) : | 37 |
| speI (ACTAGT) : | 1309 |
| sphI (GCATGC) : | 26 |
| splI (CGTACG) : | 35 |
| sse8387I (CCTGCAGG) : | 331 1351 |
| sspiI (AATATT) : | 820 853 886 919 |
| sstiI (GAGCTC) : | 1315 |
| stuiI (AGGCCT) : | 132 546 |
| styI (CCWGGG) : | 265 383 409 1024 |
| taiiI (ACGT) : | 21 38 |
| taqiI (TCGA) : | 58 1322 |
| tfiiI (GAWTC) : | 388 702 776 |
| thaiI (CGCG) : | 33 76 |
| tliiI (CTCGAG) : | 57 |
| tru9I (TTAA) : | 824 857 890 1125 1334 |
| tseiI (GCWGC) : | 89 249 375 424 427 456 487 842 875 908 |
| tsp509I (AATT) : | 50 610 1332 1336 |
| tspRI (NNCAGTGNN) : | 222 347 483 507 614 708 1033 1156 |
| vspI (ATTAAT) : | 823 856 889 1333 |
| xcmI (CCANNNNNNNNTGG) : | 802 835 868 901 |
| xhoI (CTCGAG) : | 57 |
| xhoII (RGATCY) : | 405 |
| xmaI (CCCGGG) : | 1326 |
| xmaIII (CGCCCG) : | 1300 |
| xmnI (GAANNNNTTC) : | 1331 |

not found:

acII (AACGTT), afII (CTTAAG), ahaIII (TTTAAA), alw44I (GTGCAC), apaI (GGGCCC), apaLI (GTGCAC), ascI (GGCGCGCC), aspi (GACNNNGTC),
 avaiII (ATGCAT), aviII (TGGCA), bali (TGGCA), bbrPI (CACGTG), bceAI (ACGGCNNNNNNNNNN), bfrBI (ATGCAT), bfrI (CTTAAG),
 bglII (AGATCT), bsaBI (GATNNNATC), bsiCI (TTCGAA), bsmBI (CGTCTCNNNN), bsmI (GAATGCN), bsp106 (ATCGAT), bsp120I (GGGCCC),
 bsp1407I (TGTACA), bspCI (CGATCG), bspDI (ATCGAT), bspHI (TCATGA), bsrDI (GCAATGNN), bsrGI (TGTACA), bssHII (GGCGGC),
 bssSI (CTCGTG), bst1107I (GTATAC), bst4CI (ACNGT), bstAPI (GACNNNNNGTC), bstBI (TTCGAA), bsteII (GGTNACC), bstXI (CCANNNNNNNTGG),
 bstZ17I (GTATAC), btrI (CACGTC), claI (ATCGAT), draI (TTTAAA), draII (CACNNNGTG), drdI (GACNNNNNGTC), eco72I (CACGTG),
 ecoRV (GATATC), eheI (GGCGCC), esp3I (CGTCTC), fseI (GGCCGGCC), fspI (TGCACA), hgaI (GACGC), hindIII (AAGCTT), hpyCH4III (ACNGT),
 kasI (GGCGCC), kspI (CCGCGG), maeII (GTNAC), mamI (GATNNNATC), mfeI (CAATG), mscI (TGGCCA), mslI (CAYNNNNRTG), muni (CAATTG),
 naeI (GGCGGC), narI (GGCGCC), ndeI (CATATG), ngoMI (GCCGGC), nheI (GCTAGC), nruI (TCGCA), nsiI (ATGCAT), paci (TTAATTAA),
 pflFI (GACNNNGTC), pmeI (GTTAAAC), pmlI (CACGTG), ppul0I (ATGCAT), ppulMI (RGWCCY), pshAI (GACNNNGTC), psiI (TTATAA),
 psp1406I (AACGTT), pspOMI (GGGCC), pvuI (CGATCG), rcaI (TCATGA), sacII (CCGCGG), sandI (GGWCCC), scaI (AGTACT),
 sceI (TAGGGATAACAGGGTAAT), sexAI (ACWGGT), sfiI (GGCCNNNNNGGCC), sfuI (TTCGAA), sgrAI (GCGATCG), sgrAI (CRCCGGYG),
 snoI (GTGCAC), snoI (GTGCAC), srfI (GCCCGGGC), sstII (CCGCGG), swaI (ATTTAAAT), tsp45I (GTSAC), tth11I (GACNNNGTC), xbaI (TCTAGA)